

6500922

	Preimmune	Anti-mTNF-R2	Preimmune	Anti-mTNF-R2	Preimmune	Anti-mTNF-R2	Preimmune	Anti-mTNF-R2
NF- $\kappa$ B Probe	wt	wt	mt	mt	wt	wt	wt	wt
Competitor	-	-	-	-	mt	mt	AP-1	

B ▶

F ▶

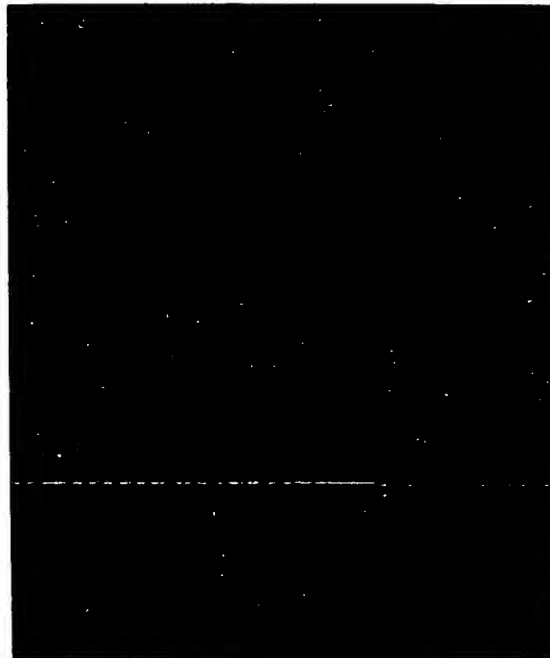


FIG. 1

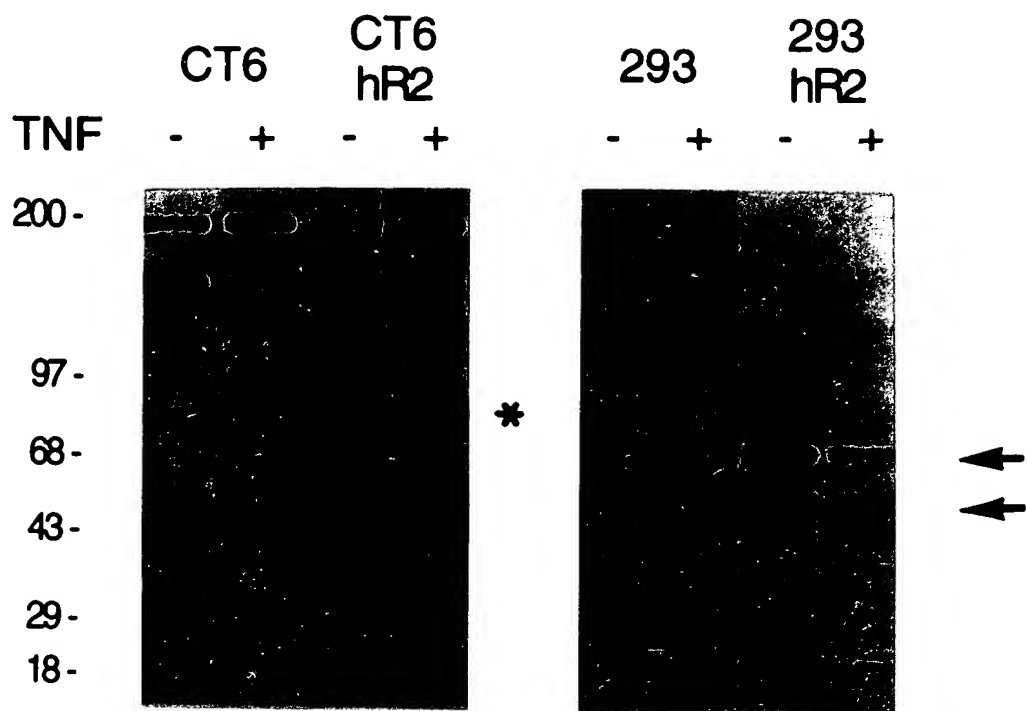


FIG. 2a

CT6  
FIG. 2b



FIG. 3

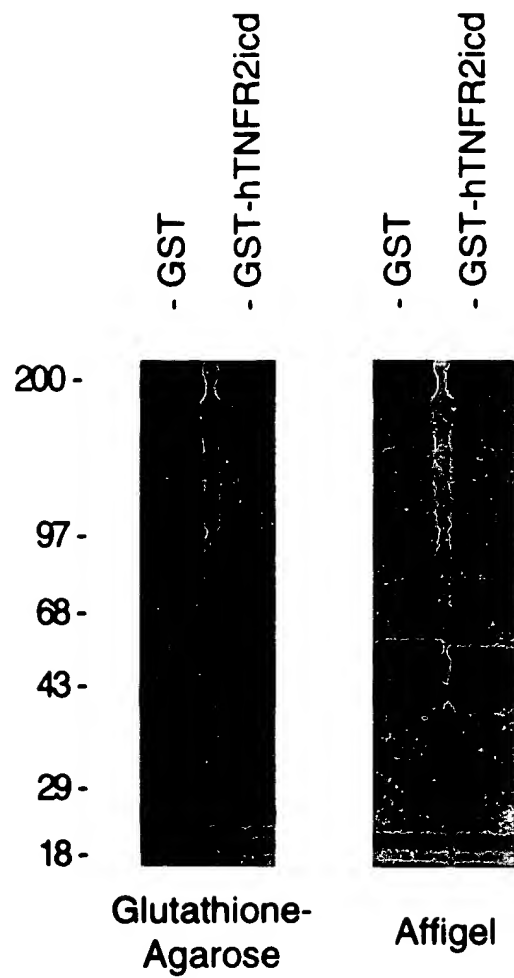


FIG. 4

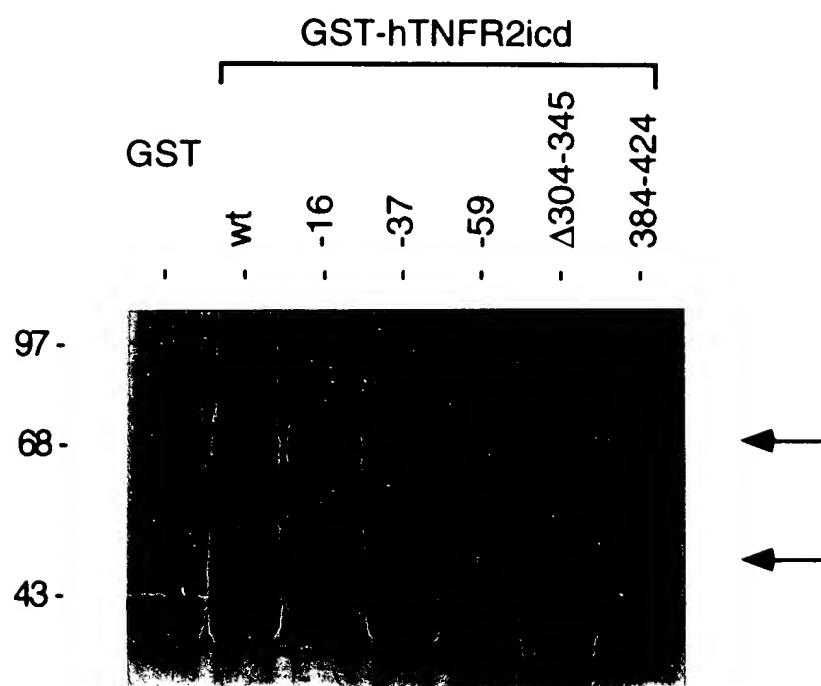


FIG. 5

	293			293-hR2				
Competitor	-	GST	wt	-	GST	wt	GST-hTNFR2icd -16 -37 -59	
	.	.	.	.	.	.	.	

FIG. 6a

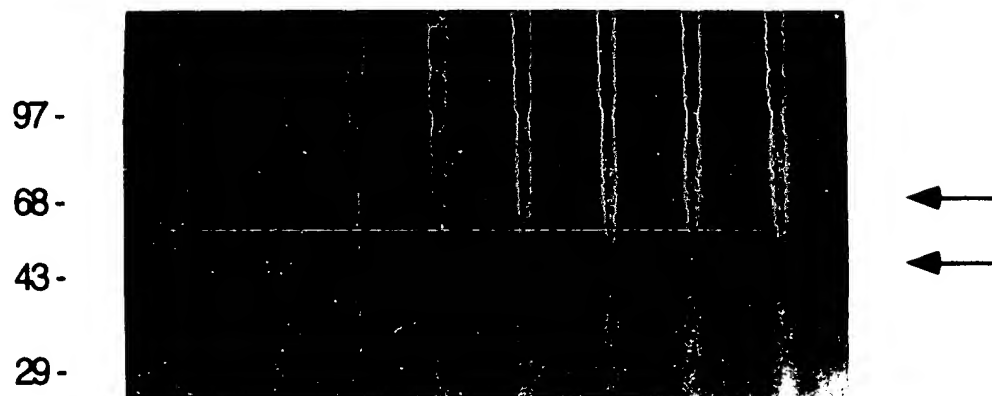


FIG. 6b



CT6

	GST		GST-hTNFR2icd	
TNF	-	+	-	+
	.	.	.	.

FIG. 7



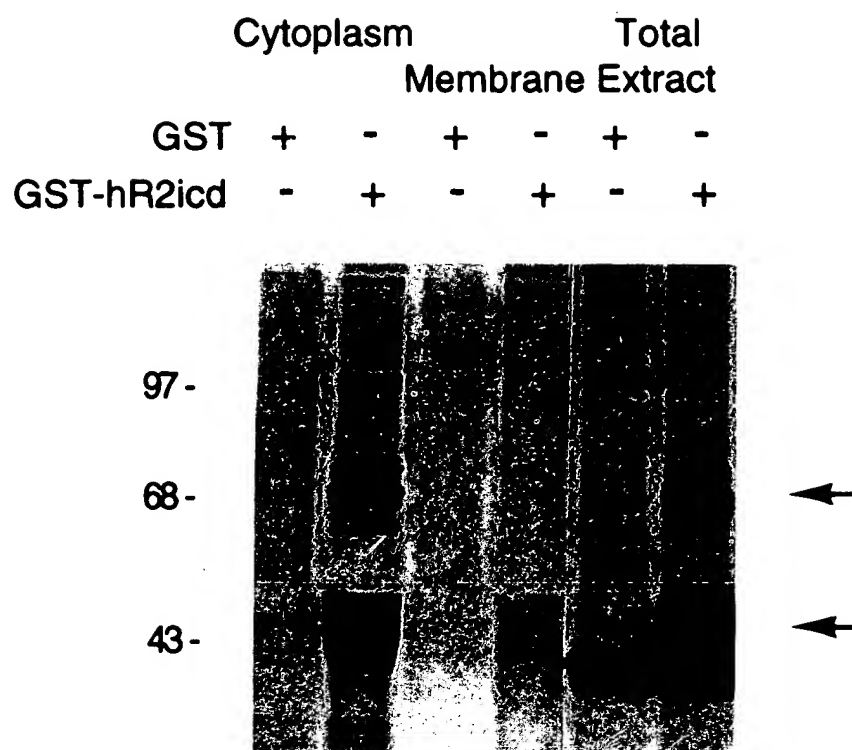


FIG. 8

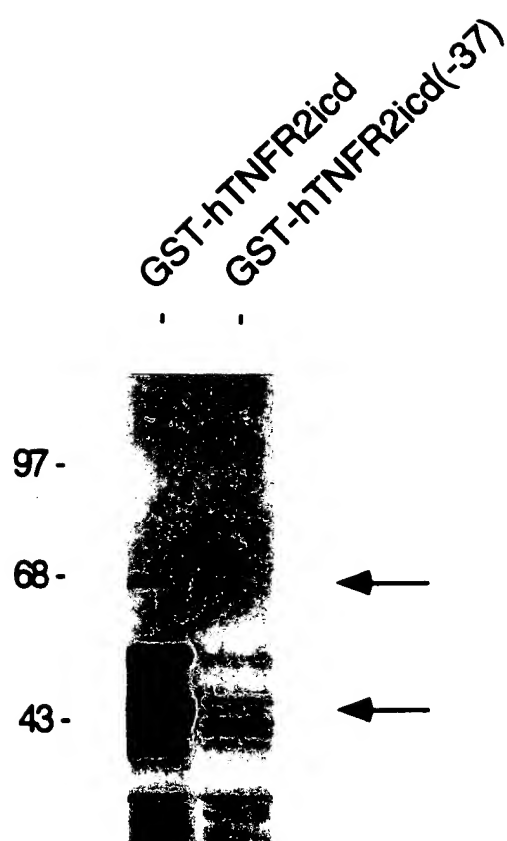


FIG. 9

1 CCCAGCCCCGGTTCTCTGCCCCCAAGGACGGCTACCGCCCCAAATGCGAGCAGAAGGCGGCGCACAGATACAGAAAGT  
74 GAGGCTCAGACATATTGAAGACCGTGTGACATAGGGTAGCCAAATGACAGTGTGAGAAAGTGACATTTACTCAAG  
149 GCCACCCAGATATCCTGGAGGACCCAGAACCTGGAGATTCCCATCAGAAAGACCCTTCTG6CCACCIGAAACCC  
1 MetAlaSerSerSerAlaProAspGluAsnGluPheGlnPheGlyCysProProAlaProCysGlnAspPro  
224 AAGATGGCCTCCAGCTCAGCCCTGATGAAACGAGTTTCAATTTGGTTGCCCCCTGCTCCCTGCCAGGACCCCA  
25 SerGluProArgValLeuCysCysThrAlaCysLeuSerGluAsnLeuArgAspGluAspArgIleCysPro  
299 TCGGAGCCACAGATTCTCTGCTGCACAGCCTGTCTCTGAGAACCTGAGAGATGATGAGGATCGGATCTGTCTCT  
50 LysCysArgAlaAspAsnLeuHisProValSerProGlySerProLeuThrGlnGluLysValHisSerAspVal  
374 AAATGCAGAGCAGACAACCTCCATCCTGTGAGCCCAGGAAGCCCTCTGACTCAGGAGAAGGTTCACTCTGATGTA  
75 AlaGluAlaGluIleMetCysProPheAlaGlyValGlyCysSerPheLysGlySerProGlnSerMetGlnGlu  
449 GCTGAGGCTGAAATCATGTGCCCTTTTGCAGGTGTTGGCTGTTCTTCAAGGGGAGCCACCAATCCATGCAAGGAG  
100 HisGluAlaThrSerGlnSerSerHisLeuTyrLeuLeuLeuAlaValLeuLysGluTrpLysSerSerProGly  
524 CATGAGGCTACCTCCCAGTCTCCACCTGTACCTGTCTGGCGGCTTTAAAGGAGTGGAAATCCTCACCAGGC  
125 SerAsnLeuGlySerAlaProMetAlaLeuGluArgAsnLeuSerGluLeuGlnLeuGlnAlaAlaValGluAla  
599 TCCAACTAGGGTCTGCACCCATGGCACTGGAGCGGAACCTGTTCAGAGCTGCAGCTTCAGGCAGCTGTGGAAAGCG  
150 ThrGlyAspLeuGluValAspCysTyrArgAlaProCysCysGluSerGlnGluGluLeuAlaLeuGlnHisLeu  
674 ACAGGGGACCTGGAGGTAGACTGCTACCGGGCACCTTGCTGTGAGAGCCAGGAAGAACTGGCCCTGCAGCACTTG  
> +  
175 ValLysGluLysLeuLeuAlaGlnLeuGluGluLysLeuArgValPheAlaAsnIleValAlaValLeuAsnLys  
749 GTGAAGGAGAAGCTGTGGCTCAGCTGGAGGAGAAGCTGCGTGTGTTTGCAACAATTGTGTCTCTCAACAAG  
200 GluValGluAlaSerHisLeuAlaLeuAlaAlaSerIleHisGlnSerGlnLeuAspArgGluHisLeuLeuSer  
824 GAAGTGGAGGCTTCCACCTGGCACCTGGCCGCCTCCATCCACCAGAGCCAGTTGGACCAGAGCACCTCCTGAGC  
225 LeuGluGlnArgValValGluLeuGlnGlnThrLeuAlaGlnLysAspGlnValLeuGlyLysLeuGluHisSer  
899 TTGGAGCAGAGGGTGTGGAAATTACAGCAAAACCCTGGCTCAAAAAGACCAGGTCTCTGGGCAAGCTTGAGCACAGT

FIG. 10a

250 LeuArgLeuMetGluGluAlaSerPheAspGlyThrPheLeuTrpLysIleThrAsnValThrLysArgCysHis  
 974 CTGCGACTCATGGAGGAGGCATCCTTTGATGGTACTTTCCCTGTGGAGATCACCAATGTACCAAGCGGTGCCAC  
  
 275 GluSerValCysGlyArgThrValSerLeuPheSerProAlaPheIyrThrAlaLysIyrGlyIyrLysLeuCys  
 1049 GAGTCAGTGTGTGGCCGGACTGTACGCCCTCTCTCTCCAGCTTTCTACACTGCCAAGTATGGTTACAAGTTGTGC  
  
 300 LeuArgLeuIyrLeuAsnGlyAspGlySerGlyLysLysThrHisLeuSerLeuPheIleValIleMetArgGly  
 1124 CTGCGCTTGTACCTGAACGGGGATGGCTCAGGCAAGAAAGACCCACCTGTCCCTCTTCATCGTGATCATGAGAGGA  
  
 325 GluTyrAspAlaLeuLeuProTrpProPheArgAsnLysValThrPheMetLeuLeuAspGlnAsnAsnArgGlu  
 1199 GAATACGATGCTCTCTGCCCTGGCCTTTCAGGAACAAGGTCACTTTATGTCTACTTGACCCAGAACAAACCGAGAG  
  
 350 HisAlaIleAspAlaPheArgProAspLeuSerSerAlaSerPheGlnArgProGlnSerGluThrAsnValAla  
 1274 CATGCTATTGATGCCCTCCGGCCTGACCTGAGCTCAGCCTCCTTCCAGCGGCCACAGAGTGAGACCAACGTGGCC  
  
 375 SerGlyCysProLeuPhePheProLeuSerLysLeuGlnSerProLysHisAlaTyrValLysAspAspThrMet  
 1349 AGCGGCTGCCCGCTCTTCTTCCCCCTCAGCAAGCTGCAGTCAACCAAGCACGCTACGTCAAAGATGACACAATG  
  
 <  
 400 PheLeuLysCysIleValAspThrSerAla  
 1424 TTCCTCAATGCATTGTGGACACTAGTGCCTTAGGGATGGGGGGAGGGGGTGTCTCTTGACAGAACCAAGCTTAGAC  
 1499 TGGGGGACTTAGCTAGACAGCCAGGCCCTGCTGCCCTTGAGGCCACAGCCACGACCAAGGAGGAGGCCAAGGCT  
 1574 GGCATGACTTCAGCGCCACAGCATGCTGGTTATGGCTGATGTGAGGCTGGAGAAACGTGTGCGTACAGAGACAGA  
 1649 GTGGAGGAGACAGAGAGTGCTCTTTTCAACACAGACTACAGACACCAAGGAGGCCAGCATGCCAGCAGCTTCTG  
 1724 AATGTTGAGACCGCCTAGATCAGGATGAAGAAGAGCCAGGCCCTGAGGCTTGGACATTTGAGCCAAGGCTATGGGGC  
 1799 CTAAAGTGAGGGGCACTCCTACCAAGGACATTTCTCTCGAGGTCAGGGCATAACTGGAAATAAGCCCTCTCTCT  
 1874 GTTCAGACTCAAAACTAGAACCAAGGAGGTCAGACATTAATGTGAATTTAACCTGCCCCTGGACTGAGT  
 1949 TCCTATGTTAACAGACACGCAACAGGTAAACCCAGAACTGCCCTGGGAAATGCTTTCTGGCTGCATCTGGAGA  
 2024 TCTTTGATGTTTTTACCGACAAACAAATAACAAAGCCTTGAAATGCAAAAAAATAAAAAA

FIG. 10b

<sup>^</sup> <sup>\*</sup> <sup>\*</sup> <sup>\*</sup>  
1 GCGCGAAGACCGTTGGGGCTTTGTGGTGTGTGGGGTTGTAACCTCACATGGCTGCAGCCAGTGTGACTTCCCCCT MetAlaAlaSerValThrSerPro  
10 GlySerLeuGluLeuLeuGlnProGlyPheSerLysThrLeuLeuGlyThrArgLeuGluAlaLysTyrLeuCys  
75 GGCTCCCTAGAACTGCTACAGCCTGGCTTCTCCAAGACCTCCTGGGACCAGGTAGAAAGCCAAAGTACCTCTGT  
35 SerAlaCysLysAsnIleLeuArgArgProPheGlnAlaGlnCysGlyHisArgTyrCysSerPheCysLeuThr  
150 TCAGCCTGCAAAACATCCTGCGAGGCCCTTCCAGGCCCAGTGTGGCACCGCTACTGCTCCTTCTGCTGACC  
60 SerIleLeuSerSerGlyProGlnAsnCysAlaAlaCysValTyrGluGlyLeuTyrGluGlyIleSerIle  
225 AGCATCCTCAGCTCTGGGCCCCAGAACTGTGCTGCCTGTGCTATGAAGGCCTGTATGAAGAGGCAATTTCTATT  
85 LeuGluSerSerSerAlaPheProAspAsnAlaAlaArgArgGluValGluSerLeuProAlaValCysProAsn  
300 TTAGAGAGTAGTTTCGGCCTTTCAGATAACGCTGCCCGCAGAGAGGTGGAGAGCCTGCCAGCTGTCTGTCCCAAT  
110 AspGlyCysThrTrpLysGlyThrLeuLysGlyTyrGluSerCysHisGluGlyLeuCysProPheLeuLeuThr  
375 GATGGATGCACCTTGGAAGGGGACCTTGAAAGAAATACGAGAGCTGCCACGAAAGGACTTTGCCCATTTCTGTGCTGACG  
135 GluCysProAlaCysLysGlyLeuValArgLeuSerGluLysGluHisThrGluGlnGluCysProLysArg  
450 GAGTGCTCCTGCATGTAAAGGCCCTGGTCCGCCCTCAGCGAGAAGGAGCACCCACACTGAGCAGGAATGCCCCCAAAGG  
160 SerLeuSerCysGlnHisCysArgAlaProCysSerHisValAspLeuGluValHisTyrGluValCysProLys  
525 AGCCTGAGCTGCCAGCAGCTGCAGAGCACCCCTGTAGCCACGTGGACCTGGAGGTACACTATGAGGTCTGCCCAAG  
185 PheProLeuThrCysAspGlyCysGlyLysLysIleProArgGluThrPheGlnAspHisValArgAlaCys  
600 TTTCCCTTAACCTGTGATGGCTGTGGCAAGAAGAAGATCCCTCGGGAGACGTTTCAGGACCATGTTAGAGCATGC  
210 SerLysCysArgValLeuCysArgPheHisThrValGlyCysSerGluMetValGluThrGluAsnLeuGlnAsp  
675 AGCAATGCCGGGTTCTCTGCAGATTCCACACCCGTTGGCTGTTCCAGAGATGGTGGAGACTGAGAACCTGCAGGAT  
235 HisGluLeuGlnArgLeuArgGluHisLeuAlaLeuLeuLeuSerSerPheLeuGluAlaGlnAlaSerProGly  
750 CATGAGCTGCAGCGGCTACGGGAACACACCTAGCCCTACTGCTGAGCTCATTTCTTGGAGGCCCAAGCCTCTCCAGGA  
260 ThrLeuAsnGlnValGlyProGluLeuLeuGlnArgCysGlnIleLeuGluGlnLysIleAlaThrPheGluAsn  
825 ACCTTGAAACCAAGGTGGGGCCAGAGCTACTCCAGCGGTGCCAGATTTTGGAGCAGAAAGATAGCAACCTTTGAGAAC

FIG. 11a



285 I l e v a l C y s v a l l e u A s n A r g G l u V a l G l u A r g V a l A l a V a l T h r A l a G l u A l a C y s S e r A r g G l n H i s A r g L e u  
900 A T T G T C T G C G T C T T G A A C C G T G A A G T A G A G A G G T A G C A G T G A C T G C A G A G G C T T G T A G C C G G C A G C A C C G G C T A  
310 A s p G l n A s p L y s I l e G l u A l a L e u S e r A s n L y s V a l G l n G l n L e u G l u A r g S e r I l e G l y L e u L y s A s p L e u A l a  
975 G A C C A G G A C A A G A T T G A G G C C C T G A G T A A C A A G G T G C A A C A G C T G G A G A G G A G C A T C G G C C T C A A G G A C C T G G C C  
335 M e t A l a A s p L e u G l u G l n L y s V a l S e r G l u L e u G l u V a l S e r T h r T y r A s p G l y V a l P h e I l e T r p L y s I l e S e r  
1050 A T G G C T G A C C T G G A G C A G A A G G T C T C C G A G T T G G A A G T A T C C A C C T A T G A T G G G G T C T T C A T C T G G A A G A T C T C T  
360 A s p P h e T h r A r g L y s A r g G l n G l u A l a V a l A l a G l y A r g T h r P r o A l a I l e P h e S e r P r o A l a P h e T y r T h r S e r  
1125 G A C T T C A C C A G A A A G C G T C A G G A A G C C G T A G T G C C G G A C A C C A G C T A T C T T C T C C C C A G C C T T C T A C A C A A G C  
385 A r g T y r G l y T y r L y s M e t C y s L e u A r g V a l T y r L e u A s n G l y A s p G l y T h r G l y A r g G l y T h r H i s L e u S e r L e u  
1200 A G A T A T G G C T A C A A G A T G T G T C T A C G A G T C T A C T T G A A T G G C G A C G G C A C T G G G C G G G A A C T C A T C T G T C T C T C  
410 P h e P h e V a l V a l M e t L y s G l y P r o A s n A s p A l a L e u L e u G l n T r p P r o P h e A s n G l n L y s V a l T h r L e u M e t L e u  
1275 T T C T T C G T G G T G A T G A A A G G C C C A A T G A T G T C T G T T G C A G T G G C C T T T T A A T C A G A A G G T A A C A T T G A T G T T G  
435 L e u A s p H i s A s n A r g G l u H i s V a l I l e A s p A l a P h e A r g P r o A s p V a l T h r S e r S e r P h e G l n A r g P r o  
1350 C T G G A C C A T A A C A A C C G G G A G C A T G T G A T C G A C G C A T T C A G G C C C G A T G T A A C C T C G T C C T C C T T C C A G A G G C C T  
460 V a l S e r A s p M e t A s n I l e A l a S e r G l y C y s P r o L e u P h e C y s P r o V a l S e r L y s M e t G l u A l a L y s A s n S e r T y r  
1425 G T C A G T G A C A T G A A C A T C G C C A G T G G C T G C C C C C T C T T C T G C C C T G T G T C C A A G A T G G A G G C C A A G A A T T C C T A T  
485 V a l A r g A s p A l a I l e P h e I l e L y s A l a I l e V a l A s p L e u T h r G l y L e u  
1500 G T G C G G G A T G A T G C G A T C T T C A T C A A A G C T A T T G T G G A C C T A A C A G G A C T C T A G C C A C C C C T G C T A A G A A T A G C A  
1575 G C T C A G T G A G G A G C T G T C A C A T T A G G C C A G C C A G G C C T G C C A C A C A C A C G G T G G G C A G G C T T G G T G T A A A T G C T G  
1650 G G G A G G C C T C A G C C T A G A G C C A A T C A C C A T C A C A C A G A A A G G A G G A A G C C T C C A G T T G G C C T T C A G C T G G  
1725 C A A C T G A G T T G A C G G T C C A C T G A G C T C A A G G C C T G G T G G A G C C G C T G G G A G C T T C T C A G C T T T C C A A T A G  
1800 G A A G C T C C T G C T G T C T G T C T G G G A A G G A G A G A C C T G T A G G T G G T G C T C A G A A A G G G C C T C T C C A G A  
1875 G A G A G T C T C A A G A G C T G C A G C A G G A A A G T A C T G G C C T T C C C A C C C C A T C C T T T G G A A A A G A G G T A G C G G C  
1950 T A C A C A G G A A A G C A T G C G C C T G C A G G G T G T A G C C C A A G A G A A G C T C T C T G A G A C A T A G G C C C T C A C T G G A G  
2025 A A G G C C T G C C T G G G C T G C A C A G C C T T G C C A G G T G G C C T G T A T G G G G G A G A A G T A A A T G T T G A G A T G T C A C  
2100 A C G A C A A A A A A A A A A A A A A A A

FIG. 11b

## FIG. 12a

TRAF2	(mouse)	31	KYL <b>C</b> SAC <b>C</b> KNILRRPFQA <b>Q</b> CGHRY <b>C</b> SF <b>C</b> LT <b>S</b> I LSS GPQN <b>C</b> AA <b>C</b> VYE
COP1	( <i>A. thaliana</i> )	49	DLL <b>C</b> PI <b>C</b> MQIIKDAFLT <b>A</b> CGHS <b>F</b> C <b>Y</b> M <b>C</b> II <b>T</b> H LRN KSD <b>C</b> PC <b>C</b> SQ <b>H</b>
EPF	(human)	10	ELS <b>C</b> SI <b>C</b> LEPFKEPVT <b>P</b> CGHNF <b>C</b> GS <b>C</b> LN <b>T</b> WA VQG SPYL <b>C</b> PQ <b>C</b> RA <b>V</b>
RAD-18	( <i>S. cerevisiae</i> )	25	LLR <b>C</b> HI <b>C</b> KDFLKVPVLT <b>P</b> CGH <b>T</b> F <b>C</b> SL <b>C</b> IR <b>T</b> H LNN QPN <b>C</b> PL <b>C</b> LF <b>E</b>
UVS-2	( <i>N. crassa</i> )	31	AFR <b>C</b> HV <b>C</b> KDFYDSPMLT <b>S</b> C <b>N</b> H <b>T</b> F <b>C</b> SL <b>C</b> IR <b>R</b> C LSV DSK <b>C</b> PL <b>C</b> RA <b>T</b>
RAG-1	(human)	290	SIS <b>C</b> QI <b>C</b> EHILADPVET <b>N</b> C <b>K</b> H <b>V</b> F <b>C</b> RV <b>C</b> IL <b>R</b> C LKV MGS <b>Y</b> C <b>P</b> S <b>C</b> CR <b>Y</b> P
SS-A/Ro	(human)	13	EVT <b>C</b> PI <b>C</b> LDLPFVEPVS <b>I</b> <b>E</b> CGHS <b>F</b> C <b>Q</b> E <b>C</b> IS <b>Q</b> V GKG GGS <b>V</b> CA <b>V</b> CR <b>Q</b> R
RING1	(human)	16	ELM <b>C</b> PI <b>C</b> LDMLKNTMTTKE <b>C</b> L <b>H</b> RF <b>C</b> SD <b>C</b> IV <b>T</b> A LRS GNKE <b>C</b> P <b>T</b> CR <b>K</b> K
RPT-1	(mouse)	12	EVT <b>C</b> PI <b>C</b> LELLKEPVSA <b>D</b> C <b>N</b> HS <b>F</b> C <b>R</b> A <b>C</b> ITL <b>N</b> YESNRNTDG <b>K</b> GN <b>C</b> PV <b>C</b> RV <b>P</b>
RFP	(human)	13	ETT <b>C</b> PV <b>C</b> LQYFAEPMML <b>D</b> CGH <b>N</b> I <b>C</b> CA <b>C</b> LARC <b>W</b> GT <b>A</b> ETNV <b>S</b> C <b>P</b> Q <b>C</b> RE <b>T</b>
c-cbl	(human)	378	FQL <b>C</b> KI <b>C</b> AENDKDVKIE <b>P</b> CGH <b>L</b> M <b>C</b> T <b>S</b> CL <b>T</b> S <b>W</b> Q <b>E</b> SE <b>G</b> Q GSS <b>G</b> C <b>P</b> F <b>C</b> CR <b>E</b>

consensus  
---C-C---X11-12---C-H-C-C---X10-16---C-C---

## FIG. 12b

TRAF2	(mouse)	157	CPKRSLS <b>C</b> QH <b>C</b> RAPCSHVDLEV <b>H</b> YE VC
		182	PKFPLT <b>C</b> DG <b>C</b> GKKKIPRETFQD <b>H</b> VR AC
DG17	( <i>D. discoideum</i> )	171	GGFKLVT <b>C</b> DF <b>C</b> KRDDIKKKELET <b>H</b> YK TC
TFIIIA	( <i>X. laevis</i> )	189	QD LAV <b>C</b> DV <b>C</b> NRKFRHKDYLRD <b>H</b> QK TH
XLCOF14	( <i>X. laevis</i> )	1	TGKYPFI <b>C</b> SE <b>C</b> GKSFMDKRYLKI <b>H</b> SN VH
XFIN	( <i>X. laevis</i> )	1225	TGEKPYT <b>C</b> TV <b>C</b> GKKFIDRSSVVK <b>H</b> SR TH
ZFY1/2	(mouse)	521	RKKFPHI <b>C</b> GE <b>C</b> GKGFRHPSALKK <b>H</b> IR VH
MFG2	(mouse)	293	SEEKPF <b>E</b> CE <b>E</b> C <b>G</b> KKFRTARHLVK <b>H</b> QR IH
RAD18	( <i>S. cerevisiae</i> )	183	PNEQMAQ <b>C</b> PI <b>C</b> QQFYPLKALEKT <b>H</b> LD EC
UVS-2	( <i>N. crassa</i> )	182	PDDGLVA <b>C</b> PI <b>C</b> LTRM KEQQVDR <b>H</b> LDTSC

TRAF2 1 MAAASVTSPGSLELLLOPGFSKTLTGTRLEAKYLC SACKNILRRPFQAQCG  
 TRAF2 51 HRYCSFCLTSILSSGPQNCAACVYEGLYEEGISILESSSAFPD NAARREV  
 TRAF2 101 ESLPAVCPNDGCTWKGT LKEYESCHEGLCPFLLTECPACKGLVRLSEKEH  
 TRAF1 1 . . . . . MASSSAPDENE FQFGCPPA  
 TRAF2 151 HTEQEC PK R S L S C Q H C R A P C S H V D L E V H Y E V C P K F P L T C D G C G K K K I P R E  
 TRAF1 20 P C O D P S E P R V L C C T A C L S E N L R D D E D R I C P K C R A D N L H P V S P G S P L T Q E  
 TRAF2 201 T F Q D H V R A C S K C R V L C R F H T V G C S E M V E T E N L O D H E L Q R L R E H L A L L L S S  
 TRAF1 69 K V H S D V . . . A E A E I M C P F A G V G C S F K G S P Q S M Q E H E A T S Q S S H L Y L L L A V  
 TRAF2 251 F L E A Q A S P G T L N Q V G P E L L Q R . . . . .  
 TRAF1 116 L K E W K S S P G S N L G S A P M A L E R N L S E L Q L Q A A V E A T G D L E V D C Y R A P C C E S  
 TRAF2 272 . . . . . C Q I L E Q K I A T F E N I V C V L N R E V E R V A V T A E A C S R Q H  
 TRAF1 166 G E E L A L O H L V K E K L L A Q L E E K L R V F A N I V A V L N K E V E A S H L A L A A S I H Q S  
 TRAF2 308 R L D Q D K I E A L S N K V Q Q L E R S I G L K D L A M A D L E Q K V S E L E V S T Y D G V F I W K  
 TRAF1 216 Q L D R E H L L S L E Q R V V E L Q O T L A Q K D Q V L G K L E H S L R L M E E A S F D G T F L W K  
 TRAF2 358 I S D F T R K R Q E A V A G R T P A I F S P A F Y T S R Y G Y K M C L R V Y L N G D G T G R G T H L  
 TRAF1 266 I T N V T K R C H E S V C G R T V S L F S P A F Y T A K Y G Y K L C L R L Y L N G D G S G K K T H L  
 TRAF2 408 S L F F V V M K G P N D A L L Q W P F N Q K V T L M L L D H N N R E H V I D A F R P D V T S S S F Q  
 TRAF1 316 S L F I V I M R G E Y D A L L P W P F R N K V T F M L L D Q N N R E H A I D A F R P D L S S A S F Q  
 TRAF2 458 R P V S D M N I A S G C P L F C P V S K M E . A K N S Y V R D D A I F I K A I V D L T G L  
 TRAF1 366 R P O S E T N V A S G C P L F F P L S K L Q S P K H A Y V K D D T M F L K C I V D T S A

FIG. 13

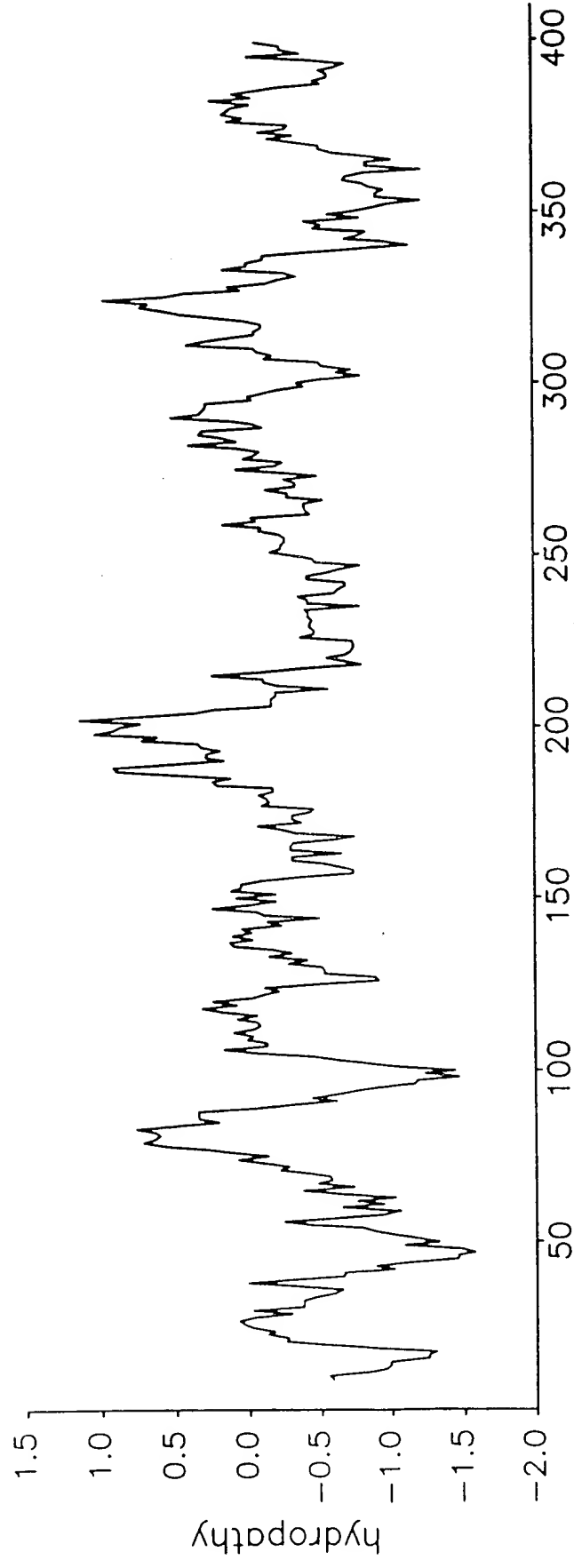


FIG. 14a

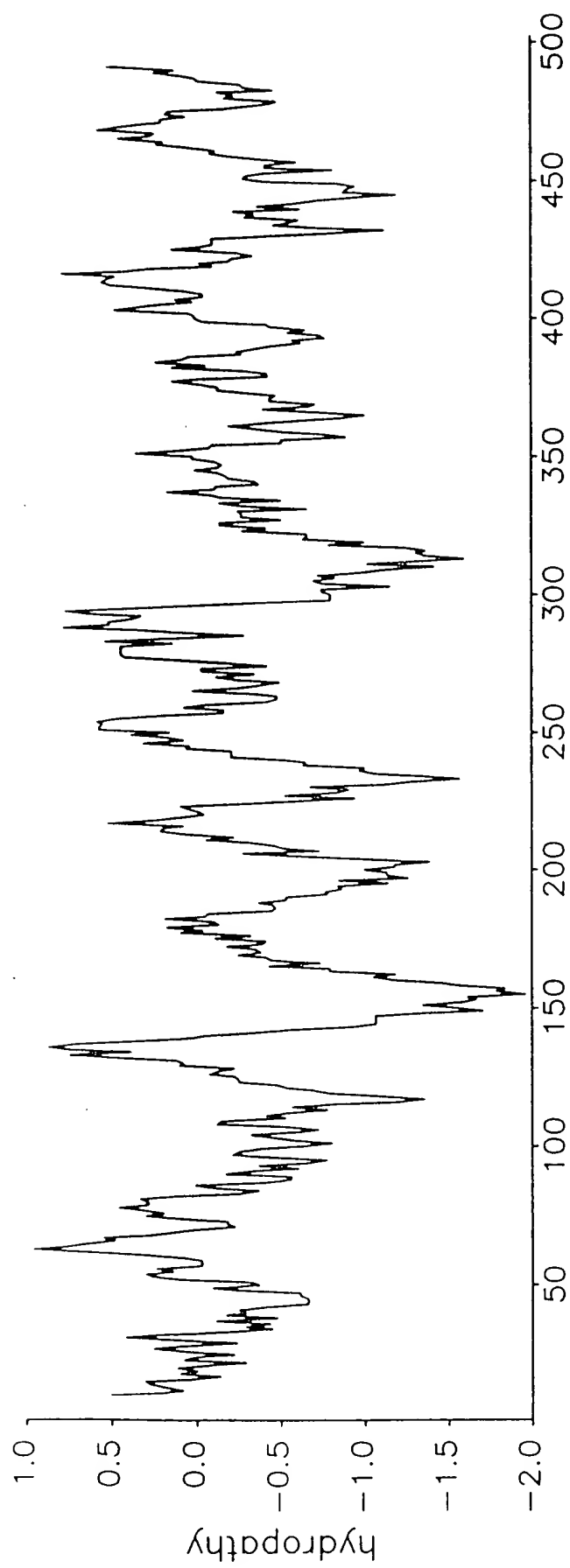


FIG. 14b

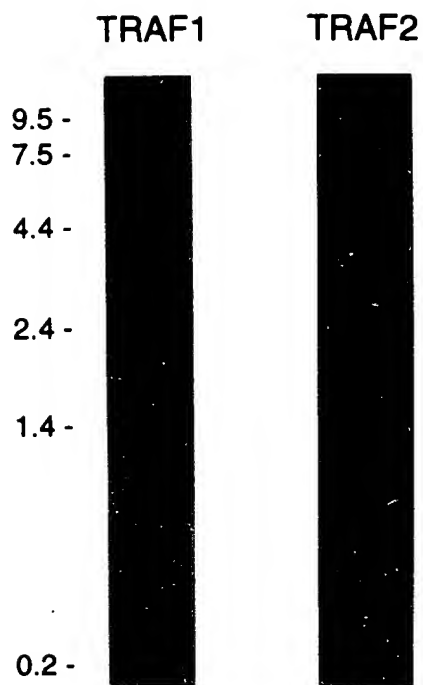


FIG. 15a

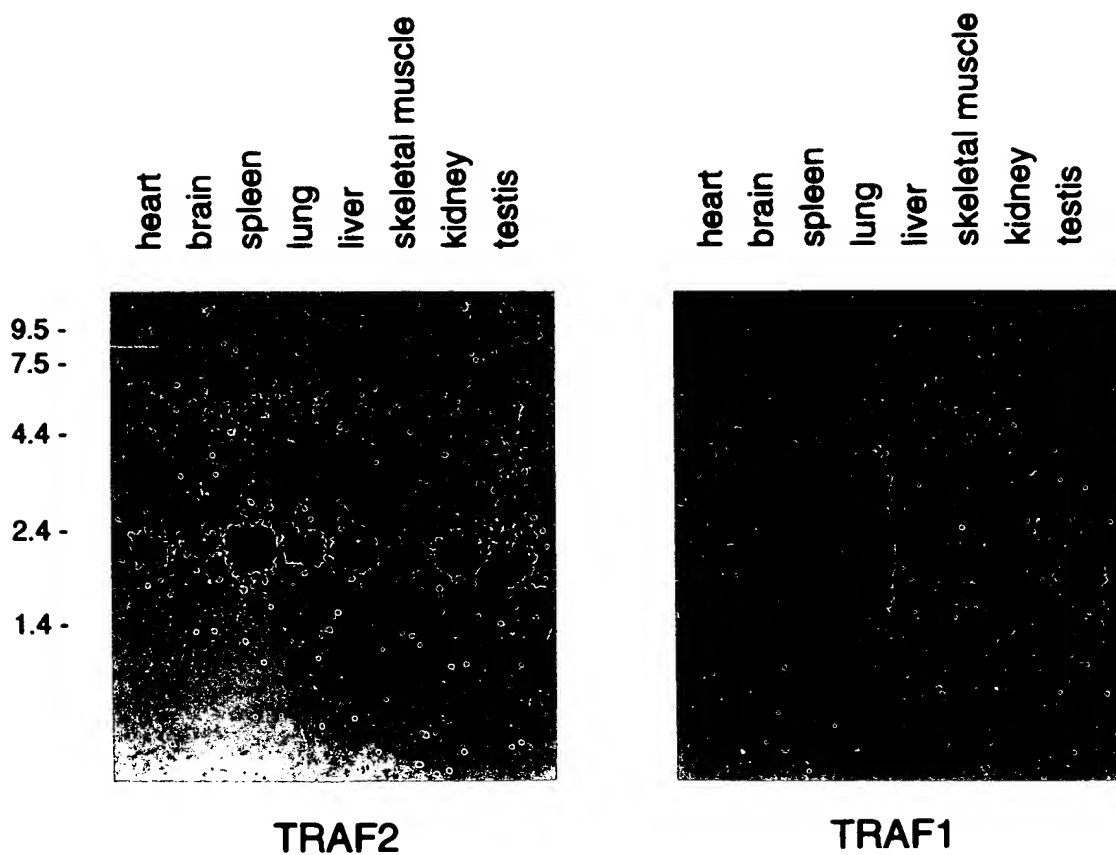


FIG. 15b

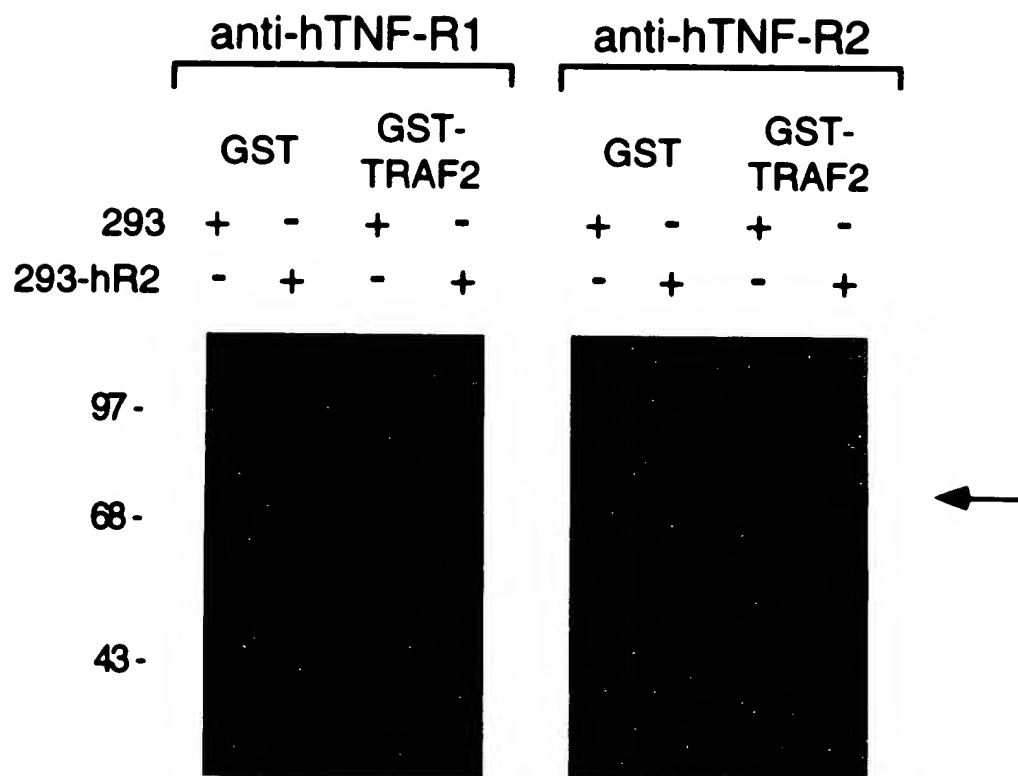


FIG. 16